

A2 OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/971,708

DATE: 10/19/2001

TIME: 10:28:50

Input Set : A:\16U 102 R1.ST25.txt

Output Set: N:\CRF3\10192001\I971708.raw

C--> 3 <110> APPLICANT: OriGene Technologies, Inc

5 <120> TITLE OF INVENTION: Human EphA6 Gene and Polypeptide

7 <130> FILE REFERENCE: OGT 16U 102 R1

C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/971,708₆₄

C--> 9 <141> CURRENT FILING DATE: 2001-10-09

9 <160> NUMBER OF SEQ ID NOS: 9

11 <170> SOFTWARE: PatentIn version 3.0

13 <210> SEQ ID NO: 1

14 <211> LENGTH: 3914

15 <212> TYPE: DNA

16 <213> ORGANISM: Homo sapien

18 <220> FEATURE:

19 <221> NAME/KEY: CDS

20 <222> LOCATION: (86)..(3196)

22 <400> SEQUENCE: 1

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29	ctt ttg caa ttt ggt ttc ttc ttg cct ctg ctg aca gcg tgg cca ggc	160
30	Leu Leu Gln Phe Gly Phe Phe Leu Pro Leu Leu Thr Ala Trp Pro Gly	
31	10 15 20 25	
33	gac tgc agt cac gtc tcc aac aac caa gtt gtg ttg ctt gat aca aca	208
34	Asp Cys Ser His Val Ser Asn Asn Gln Val Val Leu Leu Asp Thr Thr	
35	30 35 40	
37	act gta ctg gga gag cta gga tgg aaa aca tat cca tta aat ggg tgg	256
38	Thr Val Leu Gly Glu Leu Gly Trp Lys Thr Tyr Pro Leu Asn Gly Trp	
39	45 50 55	
41	gat gcc atc act gaa atg gat gaa cat aat agg ccc att cac aca tac	304
42	Asp Ala Ile Thr Glu Met Asp Glu His Asn Arg Pro Ile His Thr Tyr	
43	60 65 70	
45	cag gta tgt aat gta atg gaa cca aac caa aac aac tgg ctt cgt aca	352
46	Gln Val Cys Asn Val Met Glu Pro Asn Gln Asn Asn Trp Leu Arg Thr	
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49	aac tgg atc tcc cgt gat gca gct cag aaa att tat gtg gaa atg aaa	400
50	Asn Trp Ile Ser Arg Asp Ala Ala Gln Lys Ile Tyr Val Glu Met Lys	
51	90 95 100 105	
53	ttc aca cta agg gat tgt aac agc atc cca tgg gtc ttg ggg act tgc	448
54	Phe Thr Leu Arg Asp Cys Asn Ser Ile Pro Trp Val Leu Gly Thr Cys	
55	110 115 120	
57	aaa gaa aca ttt aat ctg ttt tat atg gaa tca gat gag tcc cac gga	496
58	Lys Glu Thr Phe Asn Leu Phe Tyr Met Glu Ser Asp Glu Ser His Gly	
59	125 130 135	
61	att aaa ttc aag cca aac cag tat aca aag atc gac aca att gct gct	544
62	Ile Lys Phe Lys Pro Asn Gln Tyr Thr Lys Ile Asp Thr Ile Ala Ala	
63	140 145 150	
65	gat gag agt ttt acc cag atg gat ttg ggt gat cgc atc ctc aaa ctc	592

ENTERED

P.5

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70 Asn Thr Glu Ile Arg Glu Val Gly Pro Ile Glu Arg Lys Gly Phe Tyr
71 170                      175                      180                      185
73 ctg gct ttt caa gac att ggg gcg tgc att gcc ctg gtt tca gtc cgt      688
74 Leu Ala Phe Gln Asp Ile Gly Ala Cys Ile Ala Leu Val Ser Val Arg
75      190                      195                      200
77 gtt ttc tac aag aaa tgc ccc ttc act gtt cgt aac ttg gcc atg ttt      736
78 Val Phe Tyr Lys Lys Cys Pro Phe Thr Val Arg Asn Leu Ala Met Phe
79      205                      210                      215
81 cct gat acc att cca agg gtt gat tcc tcc tct ttg gtt gaa gta cgg      784
82 Pro Asp Thr Ile Pro Arg Val Asp Ser Ser Ser Leu Val Glu Val Arg
83      220                      225                      230
85 ggt tct tgt gtg aag agt gct gaa gag cgt gac act cct aaa ctg tat      832
86 Gly Ser Cys Val Lys Ser Ala Glu Glu Arg Asp Thr Pro Lys Leu Tyr
87      235                      240                      245
89 tgt gga gct gat gga gat tgg ctg gtt cct ctt gga agg tgc atc tgc      880
90 Cys Gly Ala Asp Gly Asp Trp Leu Val Pro Leu Gly Arg Cys Ile Cys
91 250                      255                      260                      265
93 agt aca gga tat gaa gaa att gag ggt tct tgc cat gct tgc aga cca      928
94 Ser Thr Gly Tyr Glu Glu Ile Glu Gly Ser Cys His Ala Cys Arg Pro
95      270                      275                      280
97 gga ttc tat aaa gct ttt gct ggg aac aca aaa tgt tct aaa tgt cct      976
98 Gly Phe Tyr Lys Ala Phe Ala Gly Asn Thr Lys Cys Ser Lys Cys Pro
99      285                      290                      295
101 cca cac agt tta aca tac atg gaa gca act tct gtc tgt cag tgt gaa      1024
102 Pro His Ser Leu Thr Tyr Met Glu Ala Thr Ser Val Cys Gln Cys Glu
103      300                      305                      310
105 aag ggt tat ttc cga gct gaa aaa gac cca cct tct atg gca tgt acc      1072
106 Lys Gly Tyr Phe Arg Ala Glu Lys Asp Pro Pro Ser Met Ala Cys Thr
107      315                      320                      325
109 agg cca cct tca gct cct agg aat gtg gtt ttt aac atc aat gaa aca      1120
110 Arg Pro Pro Ser Ala Pro Arg Asn Val Val Phe Asn Ile Asn Glu Thr
111 330                      335                      340                      345
113 gcc ctt att ttg gaa tgg agc cca cca agt gac aca gga ggg aga aaa      1168
114 Ala Leu Ile Leu Glu Trp Ser Pro Pro Ser Asp Thr Gly Gly Arg Lys
115      350                      355                      360
117 gat ctc aca tac agt gta atc tgt aag aaa tgt ggc tta gac acc agc      1216
118 Asp Leu Thr Tyr Ser Val Ile Cys Lys Lys Cys Gly Leu Asp Thr Ser
119      365                      370                      375
121 cag tgt gag gac tgt ggt gga gga ctc cgc ttc atc cca aga cat aca      1264
122 Gln Cys Glu Asp Cys Gly Gly Gly Leu Arg Phe Ile Pro Arg His Thr
123      380                      385                      390
125 ggc ctg atc aac aat tcc gtg ata gta ctt gac ttt gtg tct cac gtg      1312
126 Gly Leu Ile Asn Asn Ser Val Ile Val Leu Asp Phe Val Ser His Val
127      395                      400                      405
129 aat tac acc ttt gaa ata gaa gca atg aat gga gtt tct gag ttg agt      1360
130 Asn Tyr Thr Phe Glu Ile Glu Ala Met Asn Gly Val Ser Glu Leu Ser

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131	410		415		420		425	
133	ttt tct ccc aag cca ttc aca gct att aca gtg acc acg gat caa gat	1408						
134	Phe Ser Pro Lys Pro Phe Thr Ala Ile Thr Val Thr Thr Asp Gln Asp							
135			430		435		440	
137	gca cct tcc ctg ata ggt gtg gta agg aag gac tgg gca tcc caa aat	1456						
138	Ala Pro Ser Leu Ile Gly Val Val Arg Lys Asp Trp Ala Ser Gln Asn							
139			445		450		455	
141	agc att gcc cta tca tgg caa gca cct gct ttt tcc aat gga gcc att	1504						
142	Ser Ile Ala Leu Ser Trp Gln Ala Pro Ala Phe Ser Asn Gly Ala Ile							
143			460		465		470	
145	ctg gac tac gag atc aag tac tat gag aaa gaa cat gag cag ctg acc	1552						
146	Leu Asp Tyr Glu Ile Lys Tyr Tyr Glu Lys Glu His Glu Gln Leu Thr							
147			475		480		485	
149	tac tct tcc aca agg tcc aaa gcc ccc agt gtc atc atc aca ggt ctt	1600						
150	Tyr Ser Ser Thr Arg Ser Lys Ala Pro Ser Val Ile Ile Thr Gly Leu							
151	490		495		500		505	
153	aag cca gcc acc aaa tat gta ttt cac atc cga gtg aga act gcg aca	1648						
154	Lys Pro Ala Thr Lys Tyr Val Phe His Ile Arg Val Arg Thr Ala Thr							
155			510		515		520	
157	gga tac agt ggc tac agt cag aaa ttt gaa ttt gaa aca gga gat gaa	1696						
158	Gly Tyr Ser Gly Tyr Ser Gln Lys Phe Glu Phe Glu Thr Gly Asp Glu							
159			525		530		535	
161	act tct gac atg gca gca gaa caa gga cag att ctc gtg ata gcc acc	1744						
162	Thr Ser Asp Met Ala Ala Glu Gln Gly Gln Ile Leu Val Ile Ala Thr							
163			540		545		550	
165	gcc gct gtt ggc gga ttc act ctc ctc gtc atc ctc act tta ttc ttc	1792						
166	Ala Ala Val Gly Gly Phe Thr Leu Leu Val Ile Leu Thr Leu Phe Phe							
167			555		560		565	
169	ttg atc act ggg aga tgt cag tgg tac ata aaa gcc aag atg aag tca	1840						
170	Leu Ile Thr Gly Arg Cys Gln Trp Tyr Ile Lys Ala Lys Met Lys Ser							
171	570		575		580		585	
173	gaa gag aag aga aga aac cac tta cag aat ggg cat ttg cgc ttc ccg	1888						
174	Glu Glu Lys Arg Arg Asn His Leu Gln Asn Gly His Leu Arg Phe Pro							
175			590		595		600	
177	gga att aaa act tac att gat cca gat aca tat gaa gac cca tcc cta	1936						
178	Gly Ile Lys Thr Tyr Ile Asp Pro Asp Thr Tyr Glu Asp Pro Ser Leu							
179			605		610		615	
181	gca gtc cat gaa ttt gca aag gag att gat ccc tca aga att cgt att	1984						
182	Ala Val His Glu Phe Ala Lys Glu Ile Asp Pro Ser Arg Ile Arg Ile							
183			620		625		630	
185	gag aga gtc att ggg gca ggt gaa ttt gga gaa gtc tgt agt ggg cgt	2032						
186	Glu Arg Val Ile Gly Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg							
187			635		640		645	
189	ttg aag aca cca ggg aaa aga gag atc cca gtt gcc att aaa act ttg	2080						
190	Leu Lys Thr Pro Gly Lys Arg Glu Ile Pro Val Ala Ile Lys Thr Leu							
191	650		655		660		665	
193	aaa ggt ggc cac atg gat cgg caa aga aga gat ttt cta aga gaa gct	2128						
194	Lys Gly Gly His Met Asp Arg Gln Arg Arg Asp Phe Leu Arg Glu Ala							
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199				685					690					695			
201	gtt	gtc	acc	aaa	aga	tcc	ttc	ccg	gcc	att	ggg	gtg	gag	gcg	ttt	tgc	2224
202	Val	Val	Thr	Lys	Arg	Ser	Phe	Pro	Ala	Ile	Gly	Val	Glu	Ala	Phe	Cys	
203			700					705					710				
205	ccc	agc	ttc	ctg	agg	gca	ggg	ttt	tta	aat	agc	atc	cag	gcc	ccg	cat	2272
206	Pro	Ser	Phe	Leu	Arg	Ala	Gly	Phe	Leu	Asn	Ser	Ile	Gln	Ala	Pro	His	
207		715				720				725							
209	cca	gtg	cca	ggg	gga	gga	tct	ttg	ccc	ccc	agg	att	cct	gct	ggc	aga	2320
210	Pro	Val	Pro	Gly	Gly	Gly	Ser	Leu	Pro	Pro	Arg	Ile	Pro	Ala	Gly	Arg	
211	730				735					740					745		
213	cca	gta	atg	att	gtg	gtg	gaa	tat	atg	gag	aat	gga	tcc	cta	gac	tcc	2368
214	Pro	Val	Met	Ile	Val	Val	Glu	Tyr	Met	Glu	Asn	Gly	Ser	Leu	Asp	Ser	
215				750					755					760			
217	ttt	ttg	cgg	aag	cat	gat	ggc	cac	ttc	aca	gtc	atc	cag	ttg	gtc	gga	2416
218	Phe	Leu	Arg	Lys	His	Asp	Gly	His	Phe	Thr	Val	Ile	Gln	Leu	Val	Gly	
219				765				770						775			
221	atg	ctc	cga	ggc	att	gca	tca	ggc	atg	aag	tat	ctt	tct	gat	atg	ggt	2464
222	Met	Leu	Arg	Gly	Ile	Ala	Ser	Gly	Met	Lys	Tyr	Leu	Ser	Asp	Met	Gly	
223			780					785					790				
225	tat	gtt	cat	cga	gac	cta	gcg	gct	cgg	aat	ata	ctg	gtc	aat	agc	aac	2512
226	Tyr	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Asn	Ser	Asn	
227		795				800						805					
229	tta	gta	tgc	aaa	gtt	tct	gat	ttt	ggt	ctc	tcc	aga	gtg	ctg	gaa	gat	2560
230	Leu	Val	Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Val	Leu	Glu	Asp	
231	810				815					820				825			
233	gat	cca	gaa	gct	gct	tat	aca	aca	act	ggt	gga	aaa	atc	ccc	ata	agg	2608
234	Asp	Pro	Glu	Ala	Ala	Tyr	Thr	Thr	Thr	Gly	Gly	Lys	Ile	Pro	Ile	Arg	
235				830						835				840			
237	tgg	aca	gcc	cca	gaa	gcc	atc	gcc	tac	aga	aaa	ttc	tcc	tca	gca	agc	2656
238	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Ala	Tyr	Arg	Lys	Phe	Ser	Ser	Ala	Ser	
239				845					850					855			
241	gat	gca	tgg	agc	tat	ggc	att	gtc	atg	tgg	gag	gtc	atg	tcc	tat	gga	2704
242	Asp	Ala	Trp	Ser	Tyr	Gly	Ile	Val	Met	Trp	Glu	Val	Met	Ser	Tyr	Gly	
243			860					865					870				
245	gag	aga	cct	tat	tgg	gaa	atg	tct	aac	caa	gat	gtc	att	ctg	tcc	att	2752
246	Glu	Arg	Pro	Tyr	Trp	Glu	Met	Ser	Asn	Gln	Asp	Val	Ile	Leu	Ser	Ile	
247		875					880					885					
249	gaa	gaa	ggg	tac	aga	ctt	cca	gct	ccc	atg	ggc	tgt	cca	gca	tct	cta	2800
250	Glu	Glu	Gly	Tyr	Arg	Leu	Pro	Ala	Pro	Met	Gly	Cys	Pro	Ala	Ser	Leu	
251	890					895					900				905		
253	cac	cag	ctg	atg	ctc	cac	tgc	tgg	cag	aag	gag	aga	aat	cac	aga	cca	2848
254	His	Gln	Leu	Met	Leu	His	Cys	Trp	Gln	Lys	Glu	Arg	Asn	His	Arg	Pro	
255				910						915				920			
257	aaa	ttt	act	gac	att	gtc	agc	ttc	ctt	gac	aaa	ctg	atc	cga	aat	ccc	2896
258	Lys	Phe	Thr	Asp	Ile	Val	Ser	Phe	Leu	Asp	Lys	Leu	Ile	Arg	Asn	Pro	
259				925					930					935			
261	agt	gcc	ctt	cac	acc	ctg	gtg	gag	gac	atc	ctt	gta	atg	cca	gag	tcc	2944

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266 Pro Gly Glu Val Pro Glu Tyr Pro Leu Phe Val Thr Val Gly Asp Trp
267          955          960          965
269 cta gat tct ata aag atg ggg caa tac aag aat aac ttc gtg gca gca      3040
270 Leu Asp Ser Ile Lys Met Gly Gln Tyr Lys Asn Asn Phe Val Ala Ala
271 970          975          980          985
273 ggg ttt aca aca ttt gac ctg att tca aga atg agc att gat gac att      3088
274 Gly Phe Thr Thr Phe Asp Leu Ile Ser Arg Met Ser Ile Asp Asp Ile
275          990          995          1000
277 aga aga att gga gtc ata ctt att gga cac cag aga cga ata gtc      3133
278 Arg Arg Ile Gly Val Ile Leu Ile Gly His Gln Arg Arg Ile Val
279          1005          1010          1015
281 agc agc ata cag act tta cgt tta cac atg atg cac ata cag gag      3178
282 Ser Ser Ile Gln Thr Leu Arg Leu His Met Met His Ile Gln Glu
283          1020          1025          1030
285 aag gga ttt cat gta tga aagtaccaca agcacctgtg ttttgtgcct      3226
286 Lys Gly Phe His Val
287          1035
289 cagcatttct aaaatgaacg atatcctctc tactactctc tcttctgatt ctccaaacat      3286
291 cacttcacaa actgcagtct tctgttcaga ctataggcac acacottatg tttatgcttc      3346
293 caaccaggat tttaaaatca tgctacataa atccgttctg aataacctgc aactaaaacc      3406
295 ctggcccaact gcagattatt gctacgcaat ggtaaataac tcagcatgga tgtgtaattt      3466
297 tgtataagcc gtatatggga agtgttcacg gacttaacct aaaaaaattt atccagggtg      3526
299 ggcttcctta gtgatgtatg tagagtgtga tggtagatga gaaagaacta gttgaccttt      3586
301 ctttcatggt ttgtgatcaa gtagcttcca aactgacaga aatgtttcat ttttagataa      3646
303 ttatatcag ctctattggt tgtattatta ctttattttt taataacttta actgttggtg      3706
305 cctgatattg ttagaattat ttgcagaaat gaccagtgat atcatgtaat gaatttttgt      3766
307 gaggtatgac tatggtgaga aggggggttat tagggaggga gaaaaaaata ctgtgtttat      3826
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326          20          25          30
329 Asn Gln Val Val Leu Leu Asp Thr Thr Thr Val Leu Gly Glu Leu Gly
330          35          40          45
333 Trp Lys Thr Tyr Pro Leu Asn Gly Trp Asp Ala Ile Thr Glu Met Asp
334          50          55          60
337 Glu His Asn Arg Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Glu
338 65          70          75          80
341 Pro Asn Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Arg Asp Ala
342          85          90          95

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:925 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:1010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6